SEQUENCE LISTING

<110> ONCOTHERAPY SCIENCE, INC.

      JAPAN AS REPRESENTED BY THE PRESIDENT OF THE UNIVERSITY OF TOKYO

<120> METHOD FOR DIAGNOSING COLORECTAL CANCERS

<130> ONC-X0309P

<160> 23

<170> PatentIn version 3.1

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<213> Homo sapiens

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<222> (294)..(1688)
<223>

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gctctgataa cagtcctttt ccctggcgct cacttcgtgc ctggcacccg gctgggcgcc    240

tcaagaccgt tgtctcttcg atcgcttctt tggacttggc gaccatttca gag atg      296
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tct tcc aga agt acc aaa gat tta att aaa agt aag tgg gga tcg aag        344
Ser Ser Arg Ser Thr Lys Asp Leu Ile Lys Ser Lys Trp Gly Ser Lys
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cct agt aac tcc aaa tcc gaa act aca tta gaa aaa tta aag gga gaa        392
Pro Ser Asn Ser Lys Ser Glu Thr Thr Leu Glu Lys Leu Lys Gly Glu
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att gca cac tta aag aca tca gtg gat gaa atc aca agt ggg aaa gga       440
Ile Ala His Leu Lys Thr Ser Val Asp Glu Ile Thr Ser Gly Lys Gly
        35                  40                  45


aag ctg act gat aaa gag aga cac aga ctt ttg gag aaa att cga gtc       488
Lys Leu Thr Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg Val
50                  55                  60                  65


ctt gag gct gag aag gag aag aat gct tat caa ctc aca gag aag gac       536
Leu Glu Ala Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys Asp
                    70                  75                  80


aaa gaa ata cag cga ctg aga gac caa ctg aag gcc aga tat agt act       584
Lys Glu Ile Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser Thr
                85                  90                  95


acc gca ttg ctt gaa cag ctg gaa gag aca acg aga gaa gga gaa agg       632
Thr Ala Leu Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu Arg
            100                 105                 110


agg gag cag gtg ttg aaa gcc tta tct gaa gag aaa gac gta ttg aaa       680
Arg Glu Gln Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu Lys
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3／2 0

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caa cag ttg tct gct gca acc tca cga att gct gaa ctt gaa agc aaa   728
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130   135   140   145

acc aat aca ctc cgt tta tca cag act gtg gct cca aac tgc ttc aac   776
Thr Asn Thr Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe Asn
                    150   155   160

tca tca ata aat aat att cat gaa atg gaa ata cag ctg aaa gat gct   824
Ser Ser Ile Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp Ala
                    165   170   175

ctg gag aaa aat cag cag tgg ctc gtg tat gat cag cag cgg gaa gtc   872
Leu Glu Lys Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu Val
            180   185   190

tat gta aaa gga ctt tta gca aag atc ttt gag ttg gaa aag aaa acg   920
Tyr Val Lys Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys Thr
        195   200   205

gaa aca gct gct cat tca ctc cca cag cag aca aaa aag cct gaa tca   968
Glu Thr Ala Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu Ser
210   215   220   225

gaa ggt tat ctt caa gaa gag aag cag aaa tgt tac aac gat ctc ttg   1016
Glu Gly Tyr Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu Leu
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Ala Ser Ala Lys Lys Asp Leu Glu Val Glu Arg Gln Thr Ile Thr Gln
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ctg agt ttt gaa ctg agt gaa ttt cga aga aaa tat gaa gaa acc caa   1112
Leu Ser Phe Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr Gln
        260   265   270

aaa gaa gtt cac aat tta aat cag ctg ttg tat tca caa aga agg gca   1160
Lys Glu Val His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg Ala
        275   280   285

gat gtg caa cat ctg gaa gat gat agg cat aaa aca gag aag ata caa   1208
Asp Val Gln His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile Gln
290   295   300   305

aaa ctc agg gaa gag aat gat att gct agg gga aaa ctt gaa gaa gag   1256
Lys Leu Arg Glu Glu Asn Asp Ile Ala Arg Gly Lys Leu Glu Glu Glu
                310   315   320

aag aag aga tcc gaa gag ctc tta tct cag gtc cag ttt ctt tac aca   1304
Lys Lys Arg Ser Glu Glu Leu Leu Ser Gln Val Gln Phe Leu Tyr Thr
        325   330   335

tct ctg cta aag cag caa gaa gaa caa aca agg gta gct ctg ttg gaa   1352
Ser Leu Leu Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu Glu
        340   345   350

caa cag atg cag gca tgt act tta gac ttt gaa aat gaa aaa ctc gac   1400
Gln Gln Met Gln Ala Cys Thr Leu Asp Phe Glu Asn Glu Lys Leu Asp
        355   360   365

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cgt caa cat gtg cag cat caa ttg cat gta att ctt aag gag ctc cga    1448
Arg Gln His Val Gln His Gln Leu His Val Ile Leu Lys Glu Leu Arg
370             375             380             385


aaa gca aga aat caa ata aca cag ttg gaa tcc ttg aaa cag ctt cat    1496
Lys Ala Arg Asn Gln Ile Thr Gln Leu Glu Ser Leu Lys Gln Leu His
            390             395             400


gag ttt gcc atc aca gag cca tta gtc act ttc caa gga gag act gaa    1544
Glu Phe Ala Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr Glu
        405             410             415


aac aga gaa aaa gtt gcc gcc tca cca aaa agt ccc act gct gca ctc    1592
Asn Arg Glu Lys Val Ala Ala Ser Pro Lys Ser Pro Thr Ala Ala Leu
        420             425             430


aat gaa agc ctg gtg gaa tgt ccc aag tgc aat ata cag tat cca gcc    1640
Asn Glu Ser Leu Val Glu Cys Pro Lys Cys Asn Ile Gln Tyr Pro Ala
    435             440             445


act gag cat cgc gat ctg ctt gtc cat gtg gaa tac tgt tca aag tag    1688
Thr Glu His Arg Asp Leu Leu Val His Val Glu Tyr Cys Ser Lys
450             455             460


caaaataagt atttgttttg atattaaaag attcaatact gtattttctg ttagcttgtg    1748
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cagcatgcta gtgaatcatg tatcttttag gctgctgtgc atttctcttg gcagtgatac    1868
ctccctgaca tggttcatca tcaggctgca atgacagaat gtggtgagca gcgtctactg    1928
agactactaa cattttgcac tgtcaaaata cttggtgagg aaaagatagc tcaggttatt    1988
gctaatgggt taatgcacca gcaagcaaaa tattttatgt tttgggggtt tgaaaaatca    2048
aagataatta accaaggatc ttaactgtgt tcgcattttt tatccaagca cttagaaaac    2108
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ttgtaaacca aaaactttta aatttcttca ggttttctaa catgcttacc actgggctac    2588
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<213> Homo sapiens

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Glu Ile Ala His Leu Lys Thr Ser Val Asp Glu Ile Thr Ser Gly Lys
        35   40   45

Gly Lys Leu Thr Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg
    50   55   60

Val Leu Glu Ala Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys
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65                    70                    75                    80


Asp Lys Glu Ile Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser
                85                    90                    95


Thr Thr Ala Leu Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu
                100                   105                   110


Arg Arg Glu Gln Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu
                115                   120                   125


Lys Gln Gln Leu Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser
        130                   135                   140


Lys Thr Asn Thr Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe
145                   150                   155                   160


Asn Ser Ser Ile Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp
                165                   170                   175


Ala Leu Glu Lys Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu
                180                   185                   190


Val Tyr Val Lys Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys
                195                   200                   205


Thr Glu Thr Ala Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu
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Ser Glu Gly Tyr Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu
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Leu Ala Ser Ala Lys Lys Asp Leu Glu Val Glu Arg Gln Thr Ile Thr
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Gln Leu Ser Phe Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr
              260   265   270

Gln Lys Glu Val His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg
              275   280   285

Ala Asp Val Gln His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile
     290   295   300

Gln Lys Leu Arg Glu Glu Asn Asp Ile Ala Arg Gly Lys Leu Glu Glu
305   310   315   320

Glu Lys Lys Arg Ser Glu Glu Leu Leu Ser Gln Val Gln Phe Leu Tyr
              325   330   335

Thr Ser Leu Leu Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu
              340   345   350

Glu Gln Gln Met Gln Ala Cys Thr Leu Asp Phe Glu Asn Glu Lys Leu
              355   360   365

Asp Arg Gln His Val Gln His Gln Leu His Val Ile Leu Lys Glu Leu
     370   375   380

Arg Lys Ala Arg Asn Gln Ile Thr Gln Leu Glu Ser Leu Lys Gln Leu
385   390   395   400

His Glu Phe Ala Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr
          405   410   415

Glu Asn Arg Glu Lys Val Ala Ala Ser Pro Lys Ser Pro Thr Ala Ala
          420   425   430

Leu Asn Glu Ser Leu Val Glu Cys Pro Lys Cys Asn Ile Gln Tyr Pro
          435   440   445

Ala Thr Glu His Arg Asp Leu Leu Val His Val Glu Tyr Cys Ser Lys
      450   455   460

<210> 3
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<210> 4
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<213> Artificial

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<210> 5

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<210> 8

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<210> 9

<211> 26

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<210> 11
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tggtagccaa gtgcaggtta ta   22

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<210> 13
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<210> 14
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<210> 16
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<210> 18
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<210> 21
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cttgggaggc tgaagcagaa tggcgtgaac ccgggaggcg gacgttgcag tgagccgaga    780

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aatgtgaaaa gctccgtgaa actgcagaaa cccaagccga attctgcaga tatccatcac    900

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gcgaccgagt tgctcttgcc cggcgtcaat acgggataat accgcgccac atagcagaac   4740

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aataagggcg acacggaaat gttgaatact catactcttc cttttcaat attattgaag    4980

catttatcag ggttattgtc tcatgagcgg atacatattt gaatgtattt agaaaaataa   5040

acaaataggg gttccgcgca catttccccg aaaagtgcca cctgacgtc             5089
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